SEQUENCE LISTING

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<110> Bandaru, Rajasekhar

<120> 68730 and 69112, Protein Kinase
      Molecules and Uses Therefor

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cctccccagc gcgcccccgg ccgctcctcc gcgccgcgct cgtcggcc atg gcc cgg 177
                                                      Met Ala Arg
                                                        1

gag aac ggc gag agc agc tcc tcc tgg aaa aag caa gct gaa gac atc   225
Glu Asn Gly Glu Ser Ser Ser Ser Trp Lys Lys Gln Ala Glu Asp Ile
     5   10   15

aag aag atc ttc gag ttc aaa gag acc ctc gga acc ggg gcc ttt tcc   273
Lys Lys Ile Phe Glu Phe Lys Glu Thr Leu Gly Thr Gly Ala Phe Ser
 20   25   30   35

gaa gtg gtt tta gct gaa gag aag gca act ggc aag ctc ttt gct gtg   321
Glu Val Val Leu Ala Glu Glu Lys Ala Thr Gly Lys Leu Phe Ala Val

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aag tgt atc cct aag aag gcg ctg aag ggc aag gaa agc agc ata gag    369
Lys Cys Ile Pro Lys Lys Ala Leu Lys Gly Lys Glu Ser Ser Ile Glu
            55                  60                  65

aat gag ata gcc gtc ctg aga aag att aag cat gaa aat att gtt gcc    417
Asn Glu Ile Ala Val Leu Arg Lys Ile Lys His Glu Asn Ile Val Ala
            70                  75                  80

ctg gaa gac att tat gaa agc cca aat cac ctg tac ttg gtc atg cag    465
Leu Glu Asp Ile Tyr Glu Ser Pro Asn His Leu Tyr Leu Val Met Gln
        85                  90                  95

ctg gtg tcc ggt gga gag ctg ttt gac cgg ata gtg gag aag ggg ttt    513
Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu Lys Gly Phe
100                 105                 110                 115

tat aca gag aag gat gcc agc act ctg atc cgc caa gtc ttg gac gcc    561
Tyr Thr Glu Lys Asp Ala Ser Thr Leu Ile Arg Gln Val Leu Asp Ala
                120                 125                 130

gtg tac tat ctc cac aga atg ggc atc gtc cac aga gac ctc aag ccc    609
Val Tyr Tyr Leu His Arg Met Gly Ile Val His Arg Asp Leu Lys Pro
            135                 140                 145

gaa aat ctc ttg tac tac agt caa gat gag gag tcc aaa ata atg atc    657
Glu Asn Leu Leu Tyr Tyr Ser Gln Asp Glu Glu Ser Lys Ile Met Ile
        150                 155                 160

agt gac ttt gga ttg tca aaa atg gag ggc aaa gga gat gtg atg tcc    705
Ser Asp Phe Gly Leu Ser Lys Met Glu Gly Lys Gly Asp Val Met Ser
        165                 170                 175

act gcc tgt gga act cca ggc tat gtc gct cct gaa gtc ctc gcc cag    753
Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val Leu Ala Gln
180                 185                 190                 195

aaa cct tac agc aaa gcc gtt gac tgc tgg tcc atc gga gtg att gcc    801
Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly Val Ile Ala
                200                 205                 210

tac atc ttg ctc tgc ggc tac cct cct ttt tat gat gaa aat gac tcc    849
Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu Asn Asp Ser
            215                 220                 225

aag ctc ttt gag cag atc ctc aag gcg gaa tat gag ttt gac tct ccc    897
Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe Asp Ser Pro
        230                 235                 240

tac tgg gat gac atc tcc gac tct gca aaa gac ttc att cgg aac ctg    945
Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile Arg Asn Leu
        245                 250                 255

atg gag aag gac ccg aat aaa aga tac acg tgt gag cag gca gct cgg    993
Met Glu Lys Asp Pro Asn Lys Arg Tyr Thr Cys Glu Gln Ala Ala Arg
260                 265                 270                 275

cac cca tgg atc gct ggt gac aca gcc ctc aac aaa aac atc cac gag   1041
His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asn Lys Asn Ile His Glu
                280                 285                 290

tcc gtc agc gcc cag atc cgg aaa aac ttt gcc aag agc aaa tgg aga   1089
Ser Val Ser Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser Lys Trp Arg
                295                 300                 305

caa gca ttt aat gcc acg gcc gtc gtg aga cat atg aga aaa cta cac   1137
Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg Lys Leu His
        310                 315                 320
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2

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ctc ggc agc agc ctg gac agt tca aat gca agt gtt tcg agc agc ctc   1185
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agt ttg gcc agc caa aaa gac tgt gcg tat gta gca aaa cca gaa tcc   1233
Ser Leu Ala Ser Gln Lys Asp Cys Ala Tyr Val Ala Lys Pro Glu Ser
340             345             350             355

ctc agc tga cactgaagac gagcctgggg tggagaggag ggagccggca           1282
Leu Ser *


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Ala Phe Ser Glu Val Val Leu Ala Glu Glu Lys Ala Thr Gly Lys Leu
        35              40              45
Phe Ala Val Lys Cys Ile Pro Lys Lys Ala Leu Lys Gly Lys Glu Ser
    50              55              60
Ser Ile Glu Asn Glu Ile Ala Val Leu Arg Lys Ile Lys His Glu Asn
65              70              75              80
Ile Val Ala Leu Glu Asp Ile Tyr Glu Ser Pro Asn His Leu Tyr Leu
                85              90              95
Val Met Gln Leu Val Ser Gly Gly Glu Leu Phe Asp Arg Ile Val Glu
            100             105             110
Lys Gly Phe Tyr Thr Glu Lys Asp Ala Ser Thr Leu Ile Arg Gln Val
        115             120             125
Leu Asp Ala Val Tyr Tyr Leu His Arg Met Gly Ile Val His Arg Asp
    130             135             140
Leu Lys Pro Glu Asn Leu Leu Tyr Tyr Ser Gln Asp Glu Glu Ser Lys
145             150             155             160
Ile Met Ile Ser Asp Phe Gly Leu Ser Lys Met Glu Gly Lys Gly Asp
                165             170             175
Val Met Ser Thr Ala Cys Gly Thr Pro Gly Tyr Val Ala Pro Glu Val
            180             185             190
Leu Ala Gln Lys Pro Tyr Ser Lys Ala Val Asp Cys Trp Ser Ile Gly
        195             200             205
Val Ile Ala Tyr Ile Leu Leu Cys Gly Tyr Pro Pro Phe Tyr Asp Glu
210             215             220
Asn Asp Ser Lys Leu Phe Glu Gln Ile Leu Lys Ala Glu Tyr Glu Phe
225             230             235             240
Asp Ser Pro Tyr Trp Asp Asp Ile Ser Asp Ser Ala Lys Asp Phe Ile
                245             250             255
Arg Asn Leu Met Glu Lys Asp Pro Asn Lys Arg Tyr Thr Cys Glu Gln
            260             265             270
Ala Ala Arg His Pro Trp Ile Ala Gly Asp Thr Ala Leu Asn Lys Asn
        275             280             285
Ile His Glu Ser Val Ser Ala Gln Ile Arg Lys Asn Phe Ala Lys Ser
    290             295             300
Lys Trp Arg Gln Ala Phe Asn Ala Thr Ala Val Val Arg His Met Arg
305             310             315             320
Lys Leu His Leu Gly Ser Ser Leu Asp Ser Ser Asn Ala Ser Val Ser
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3

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Pro Glu Ser Leu Ser
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gtccacagag acctcaagcc cgaaaatctc ttgtactaca gtcaagatga ggagtccaaa 480
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gagaaggacc cgaataaaag atacacgtgt gagcaggcag ctcggcaccc atggatcgct 840
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tacattaaaa acaaccctga tatcaagcca gttgaaaatg gaccttggag ggaaaaagta 180
cgagaaacca tgaaggatca agttcagcga aatgaggaca aatctactac cttgaaattg 240
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gctttcatag ct atg ggc aaa gaa cca ctg aca ctg aag agc att cag gtg 1251
            Met Gly Lys Glu Pro Leu Thr Leu Lys Ser Ile Gln Val
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4

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gct gta gaa gaa ctg tac ccc aac aaa gcc cgg gcc ctg aca ctg gcc    1299
Ala Val Glu Glu Leu Tyr Pro Asn Lys Ala Arg Ala Leu Thr Leu Ala
        15              20              25

cag cac agc cgt gcc cct tct cca agg ctg agg agc agg ctg ttt agc    1347
Gln His Ser Arg Ala Pro Ser Pro Arg Leu Arg Ser Arg Leu Phe Ser
 30              35              40              45

aag gct ctg aaa gga gac cac cgc tgt ggg gag acc gag acc ccc aag    1395
Lys Ala Leu Lys Gly Asp His Arg Cys Gly Glu Thr Glu Thr Pro Lys
            50              55              60

agc tgc agc gaa gtt gca gga tgc aag gca gcc atg agg cac cag ggg    1443
Ser Cys Ser Glu Val Ala Gly Cys Lys Ala Ala Met Arg His Gln Gly
                65              70              75

aag atc ccc gag gag ctt tca cta gat gac aga gcg agg acc cag aag    1491
Lys Ile Pro Glu Glu Leu Ser Leu Asp Asp Arg Ala Arg Thr Gln Lys
            80              85              90

aag tgg ggg agg ggg aaa tgg gag cca gaa ccc agt agc aag ccc ccc    1539
Lys Trp Gly Arg Gly Lys Trp Glu Pro Glu Pro Ser Ser Lys Pro Pro
        95              100             105

agg gaa gcc act ctg gaa gag agg cac gca agg gga gag aag cat ctt    1587
Arg Glu Ala Thr Leu Glu Glu Arg His Ala Arg Gly Glu Lys His Leu
110             115             120             125

ggg gtg gag att gaa aag acc tcg ggt gaa att atc aga tgc gag aag    1635
Gly Val Glu Ile Glu Lys Thr Ser Gly Glu Ile Ile Arg Cys Glu Lys
                130             135             140

tgc aag aga gag agg gag ctc cag cag agc ctg gag cgt gag agg ctt    1683
Cys Lys Arg Glu Arg Glu Leu Gln Gln Ser Leu Glu Arg Glu Arg Leu
            145             150             155

tct ctg ggg acc agt gag ctg gat atg ggg aag ggc cca atg tat gat    1731
Ser Leu Gly Thr Ser Glu Leu Asp Met Gly Lys Gly Pro Met Tyr Asp
            160             165             170

gtg gag aag ctg gtg agg acc aga agc tgc agg agg tct ccc gag gca    1779
Val Glu Lys Leu Val Arg Thr Arg Ser Cys Arg Arg Ser Pro Glu Ala
175             180             185

aat cct gca agt ggg gag gaa ggg tgg aag ggt gac agc cac agg agc    1827
Asn Pro Ala Ser Gly Glu Glu Gly Trp Lys Gly Asp Ser His Arg Ser
190             195             200             205

agc ccc agg aat ccc act caa gag ctg agg aga ccc agc aag agc atg    1875
Ser Pro Arg Asn Pro Thr Gln Glu Leu Arg Arg Pro Ser Lys Ser Met
            210             215             220

gac aag aaa gag gac aga ggc cca gag gat caa gaa agc cat gct cag    1923
Asp Lys Lys Glu Asp Arg Gly Pro Glu Asp Gln Glu Ser His Ala Gln
            225             230             235

gga gca gcc aag gcc aag aag gac ctt gtg gaa gtt ctt cct gtc aca    1971
Gly Ala Ala Lys Ala Lys Lys Asp Leu Val Glu Val Leu Pro Val Thr
            240             245             250

gag gag ggg ctg agg gag gtg aag aag gac acc agg ccc atg agc agg    2019
Glu Glu Gly Leu Arg Glu Val Lys Lys Asp Thr Arg Pro Met Ser Arg
255             260             265

agc aaa cat ggt ggc tgg ctc ctg aga gag cac cag gcg ggc ttt gag    2067
Ser Lys His Gly Gly Trp Leu Leu Arg Glu His Gln Ala Gly Phe Glu
270             275             280             285

aag ctc cgc agg acc cga gga gaa gag aag gag gca gag aag gag aaa    2115
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5

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Lys Leu Arg Arg Thr Arg Gly Glu Glu Lys Glu Ala Glu Lys Glu Lys
              290                 295                 300

aag cca tgt atg tct gga ggc aga agg atg act ctc aga gat gac caa   2163
Lys Pro Cys Met Ser Gly Gly Arg Arg Met Thr Leu Arg Asp Asp Gln
            305                         310                 315

cct gca aag cta gaa aag gag ccc aag acg agg cca gaa gag aac aag   2211
Pro Ala Lys Leu Glu Lys Glu Pro Lys Thr Arg Pro Glu Glu Asn Lys
            320                 325                 330

cca gag cgg ccc agc ggt cgg aag cca cgg ccc atg ggc atc att gcc   2259
Pro Glu Arg Pro Ser Gly Arg Lys Pro Arg Pro Met Gly Ile Ile Ala
        335                 340                 345

gcc aat gtg gaa aag cat tat gag act ggc cgg gtc att ggg gat ggg   2307
Ala Asn Val Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly Asp Gly
350                 355                 360                 365

aac ttt gct gtc gtg aag gag tgc aga cac cgc gag acc agg cag gcc   2355
Asn Phe Ala Val Val Lys Glu Cys Arg His Arg Glu Thr Arg Gln Ala
                370                 375                 380

tat gcg atg aag atc att gac aag tcc aga ctc aag ggc aag gag gac   2403
Tyr Ala Met Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys Glu Asp
            385                 390                 395

atg gtg gac agt gag atc ttg atc atc cag agc ctc tct cac ccc aac   2451
Met Val Asp Ser Glu Ile Leu Ile Ile Gln Ser Leu Ser His Pro Asn
            400                 405                 410

atc gtg aaa ttg cat gaa gtc tac gaa aca gac atg gaa atc tac ctg   2499
Ile Val Lys Leu His Glu Val Tyr Glu Thr Asp Met Glu Ile Tyr Leu
        415                 420                 425

atc ctg gag tac gtg cag gga gga gac ctt ttt gac gcc atc ata gaa   2547
Ile Leu Glu Tyr Val Gln Gly Gly Asp Leu Phe Asp Ala Ile Ile Glu
430                 435                 440                 445

agt gtg aag ttc ccg gag ccc gat gct gcc ctc atg atc atg gac tta   2595
Ser Val Lys Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met Asp Leu
                450                 455                 460

tgc aaa gcc ctc gtc cac atg cac gac aag agc att gtc cac cgg gac   2643
Cys Lys Ala Leu Val His Met His Asp Lys Ser Ile Val His Arg Asp
            465                 470                 475

ctc aag ccg gaa aac ctt ttg gtt cag cga aat gag gac aaa tct act   2691
Leu Lys Pro Glu Asn Leu Leu Val Gln Arg Asn Glu Asp Lys Ser Thr
            480                 485                 490

acc ttg aaa ttg gct gat ttt gga ctt gca aag cat gtg gtg aga cct   2739
Thr Leu Lys Leu Ala Asp Phe Gly Leu Ala Lys His Val Val Arg Pro
            495                 500                 505

ata ttt act gtg tgt ggg acc cca act tac gta gct ccc gaa att ctt   2787
Ile Phe Thr Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu Ile Leu
510                 515                 520                 525

tct gag aaa ggt tat gga ctg gag gtg gac atg tgg gct gct ggc gtg   2835
Ser Glu Lys Gly Tyr Gly Leu Glu Val Asp Met Trp Ala Ala Gly Val
                530                 535                 540

atc ctc tat atc ctg ctg tgt ggc ttt ccc cca ttc cgc agc cct gag   2883
Ile Leu Tyr Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser Pro Glu
            545                 550                 555

agg gac cag gac gag ctc ttt aac atc atc cag ctg ggc cac ttt gag   2931
Arg Asp Gln Asp Glu Leu Phe Asn Ile Ile Gln Leu Gly His Phe Glu
        560                 565                 570
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6

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ttc ctc ccc cct tac tgg gac aat atc tct gat gct gct aaa gat ctg      2979
Phe Leu Pro Pro Tyr Trp Asp Asn Ile Ser Asp Ala Ala Lys Asp Leu
·   575                     ·   580                 585

gtg agc cgg ttg ctg gtg gta gac ccc aaa aag cgc tac aca gct cat      3027
Val Ser Arg Leu Leu Val Val Asp Pro Lys Lys Arg Tyr Thr Ala His
590                     595                 600                 605

cag gtt ctt cag cac ccc tgg atc gaa aca gct ggc aag acc aat aca      3075
Gln Val Leu Gln His Pro Trp Ile Glu Thr Ala Gly Lys Thr Asn Thr
                    610                 615                 620

gtg aaa cga cag aag cag gtg tcc ccc agc agc gag ggt cac ttc cgg      3123
Val Lys Arg Gln Lys Gln Val Ser Pro Ser Ser Glu Gly His Phe Arg
                625                 630                 635

agc cag cac aag agg gtt gtg gag cag gta tca tag tcaccacctt          3169
Ser Gln His Lys Arg Val Val Glu Gln Val Ser *
            640                 645

gggaatctgt ccagcccca gttctgctca aggacagaga aaaggataga agtttgagag 3229
aaaaacaatg aaagaggctt cttcacataa ttggtgaatc agagggagag acactgagta 3289
tattttaaag catattaaaa aaattaagtc aatgttaaat gtcacaacat atttttagat 3349
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agtggtgctt accagggtct aaactccccc tgtgagatta ataaggtgca ttgtggtctt 3529
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            20                  25                  30
Arg Ala Pro Ser Pro Arg Leu Arg Ser Arg Leu Phe Ser Lys Ala Leu
        35                  40                  45
Lys Gly Asp His Arg Cys Gly Glu Thr Glu Thr Pro Lys Ser Cys Ser
        50                  55                  60
Glu Val Ala Gly Cys Lys Ala Ala Met Arg His Gln Gly Lys Ile Pro
65                  70                  75                  80
Glu Glu Leu Ser Leu Asp Asp Arg Ala Arg Thr Gln Lys Lys Trp Gly
                85                  90                  95
Arg Gly Lys Trp Glu Pro Glu Pro Ser Ser Lys Pro Pro Arg Glu Ala
                100                 105                 110
Thr Leu Glu Glu Arg His Ala Arg Gly Glu Lys His Leu Gly Val Glu
            115                 120                 125
Ile Glu Lys Thr Ser Gly Glu Ile Ile Arg Cys Glu Lys Cys Lys Arg
    130                 135                 140
Glu Arg Glu Leu Gln Gln Ser Leu Glu Arg Glu Arg Leu Ser Leu Gly
145                 150                 155                 160
Thr Ser Glu Leu Asp Met Gly Lys Gly Pro Met Tyr Asp Val Glu Lys
                165                 170                 175
Leu Val Arg Thr Arg Ser Cys Arg Arg Ser Pro Glu Ala Asn Pro Ala
            180                 185                 190
Ser Gly Glu Glu Gly Trp Lys Gly Asp Ser His Arg Ser Ser Pro Arg
        195                 200                 205
Asn Pro Thr Gln Glu Leu Arg Arg Pro Ser Lys Ser Met Asp Lys Lys
    210                 215                 220
Glu Asp Arg Gly Pro Glu Asp Gln Glu Ser His Ala Gln Gly Ala Ala
225                 230                 235                 240
Lys Ala Lys Lys Asp Leu Val Glu Val Leu Pro Val Thr Glu Glu Gly
                245                 250                 255
Leu Arg Glu Val Lys Lys Asp Thr Arg Pro Met Ser Arg Ser Lys His
            260                 265                 270
Gly Gly Trp Leu Leu Arg Glu His Gln Ala Gly Phe Glu Lys Leu Arg
```

7

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              275                      280                      285
    Arg Thr Arg Gly Glu Glu Lys Glu Ala Glu Lys Glu Lys Lys Pro Cys
        290                      295                      300
   ·Met Ser Gly Gly Arg Arg Met Thr Leu Arg Asp Asp Gln Pro Ala Lys
    305                      310                      315                      320
    Leu Glu Lys Glu ·Pro Lys Thr Arg Pro Glu Glu Asn Lys Pro Glu Arg
                     325                      330                      335
    Pro Ser Gly Arg Lys Pro Arg Pro Met Gly Ile Ile Ala Ala Asn Val
            340                      345                      350
    Glu Lys His Tyr Glu Thr Gly Arg Val Ile Gly Asp Gly Asn Phe Ala
        355                      360                      365
    Val Val Lys Glu Cys Arg His Arg Glu Thr Arg Gln Ala Tyr Ala Met
        370                      375                      380
    Lys Ile Ile Asp Lys Ser Arg Leu Lys Gly Lys Glu Asp Met Val Asp
    385                      390                      395                      400
    Ser Glu Ile Leu Ile Ile Gln Ser Leu Ser His Pro Asn Ile Val Lys
                     405                      410                      415
    Leu His Glu Val Tyr Glu Thr Asp Met Glu Ile Tyr Leu Ile Leu Glu
            420                      425                      430
    Tyr Val Gln Gly Gly Asp Leu Phe Asp Ala Ile Ile Glu Ser Val Lys
            435                      440                      445
    Phe Pro Glu Pro Asp Ala Ala Leu Met Ile Met Asp Leu Cys Lys Ala
        450                      455                      460
    Leu Val His Met His Asp Lys Ser Ile Val His Arg Asp Leu Lys Pro
    465                      470                      475                      480
    Glu Asn Leu Leu Val Gln Arg Asn Glu Asp Lys Ser Thr Thr Leu Lys
                     485                      490                      495
    Leu Ala Asp Phe Gly Leu Ala Lys His Val Val Arg Pro Ile Phe Thr
            500                      505                      510
    Val Cys Gly Thr Pro Thr Tyr Val Ala Pro Glu Ile Leu Ser Glu Lys
        515                      520                      525
    Gly Tyr Gly Leu Glu Val Asp Met Trp Ala Ala Gly Val Ile Leu Tyr
        530                      535                      540
    Ile Leu Leu Cys Gly Phe Pro Pro Phe Arg Ser Pro Glu Arg Asp Gln
    545                      550                      555                      560
    Asp Glu Leu Phe Asn Ile Ile Gln Leu Gly His Phe Glu Phe Leu Pro
                     565                      570                      575
    Pro Tyr Trp Asp Asn Ile Ser Asp Ala Ala Lys Asp Leu Val Ser Arg
            580                      585                      590
    Leu Leu Val Val Asp Pro Lys Lys Arg Tyr Thr Ala His Gln Val Leu
            595                      600                      605
    Gln His Pro Trp Ile Glu Thr Ala Gly Lys Thr Asn Thr Val Lys Arg
        610                      615                      620
    Gln Lys Gln Val Ser Pro Ser Ser Glu Gly His Phe Arg Ser Gln His
    625                      630                      635                      640
    Lys Arg Val Val Glu Gln Val Ser
                     645
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agcaggctgt ttagcaaggc tctgaaagga gaccaccgct gtggggagac cgagaccccc  180
aagagctgca gcgaagttgc aggatgcaag gcagccatga ggcaccaggg gaagatcccc  240
gaggagcttt cactagatga cagagcgagg acccagaaga agtgggggag ggggaaatgg  300
gagccagaac ccagtagcaa gcccccaggg gaagccactc tggaagagag gcacgcaagg  360
ggagagaagc atcttggggt ggagattgaa aagacctcgg gtgaaattat cagatgcgag  420
aagtgcaaga gagagaggga gctccagcag agcctggagc gtgagaggct ttctctgggg  480
accagtgagc tggatatggg gaagggccca atgtatgatg tggagaagct ggtgaggacc  540
agaagctgca ggaggtctcc cgaggcaaat cctgcaagtg gggaggaagg gtggaagggt  600
gacagccaca ggagcagccc caggaatccc actcaagagc tgaggagacc cagcaagagc  660
atggacaaga aagaggacag aggcccagag gatcaagaaa gccatgctca gggagcagcc  720
aaggccaaga aggaccttgt ggaagttctt cctgtcacag aggagggct gagggaggtg  780
aagaaggaca ccaggcccat gagcaggagc aaacatggtg ctggctcct gagagagcac  840
caggcgggct ttgagaagct ccgcaggacc cgaggagaag agaaggaggc agagaaggag  900
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ggacttgcaa agcatgtggt gagacctata tttactgtgt gtgggacccc aacttacgta 1560
gctcccgaaa ttctttctga gaaaggttat ggactggagg tggacatgtg ggctgctggc 1620
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cgctacacag ctcatcaggt tcttcagcac ccctggatcg aaacagctgg caagaccaat 1860
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<210> 7
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence involved in ATP binding
       (Prosite Accession No. PS00107)

<221> VARIANT
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<223> Leu can be Ile or Val.

<221> VARIANT
<222> 3
<223> Xaa can be any amino acid except Pro.

<221> VARIANT
<222> 5
<223> Xaa can be any amino acid except Pro.

<221> VARIANT
<222> 6
<223> Phe can be Tyr, Trp, Met, Gly, Ser, Thr, Asn, or
       His.

<221> VARIANT
<222> 7
<223> Ser can be Gly or Ala.

<221> VARIANT
<222> (8)...(8)
<223> Xaa can be any amino acid except Pro or Trp.

<221> VARIANT
<222> (9)...(9)
<223> Leu can be Ile, Val, Cys, Ala, or Thr.

<221> VARIANT
<222> (10)...(10)
<223> Xaa can be any amino acid except Pro or Asp.

<221> VARIANT
<222> (11)...(11)
<223> Xaa can be any amino acid.

<221> VARIANT
<222> (12)...(12)
<223> Gly can be Ser, Thr, Ala, Cys, Leu, Ile, Val, Met,
       Phe, or Tyr.

9

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<221> VARIANT
<222> (13)...(13)
<223> Xaa can be any amino acid and asfew as 5 and as
      many as 18 amino acids.

<221> VARIANT
<222> (14)...(14)
<223> Leu can be Ile, Val, Met, Phe, Tyr, Trp, Cys, Ser,
      Thr, Ala, or Arg.

<221> VARIANT
<222> (15)...(15)
<223> Ala can be Ile, Val, or Pro.

<221> VARIANT
<222> (16)...(16)
<223> Leu can be Ile, Val, Met, Phe, Ala, Gly, Cys. Lys,
      or Arg.

<221> BINDING
<222> (17)...(17)

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Lys
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<210> 8
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence for serine/threonine kinases
      (Prosite Accession No. PS00108)

<221> VARIANT
<222> 1
<223> Leu can be Ile, Val, Met, Phe, or Tyr

<221> VARIANT
<222> 2
<223> Xaa can be any amino acid.

<221> VARIANT
<222> 3
<223> His can be Tyr.

<221> VARIANT
<222> 4
<223> Xaa can be any amino acid.

<221> ACT_SITE
<222> 5

<221> VARIANT
<222> (6)...(6)
<223> Leu can be Ile, Val, Met, Phe, or Tyr.

<221> VARIANT
<222> (8)...(9)
<223> Xaa can be any amino acid.

<221> VARIANT
<222> (11)...(11)
<223> Leu can be Ile, Val, Met, Phe, Tyr, Cys, or Thr.
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<221> VARIANT
<222> (12)...(12)
<223> Leu can be Ile, Val, Met, Phe, Tyr, Cys, or Thr.

<221> VARIANT
<222> (13)...(13)
<223> Leu can be Ile, Val, Met, Phe, Tyr, Cys, or Thr.

<400> 8
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 1               5                  10


<210> 9
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence for tyrosine kinase (Prosite
      Accession No. PS00109;

<221> VARIANT
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<223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.

<221> VARIANT
<222> 2
<223> Xaa can be any amino acid.

<221> VARIANT
<222> 3
<223> His can be Tyr.

<221> VARIANT
<222> 4
<223> Xaa can be any amino acid.

<221> ACT_SITE
<222> 5

<221> VARIANT
<222> (6)...(6)
<223> Leu can be Ile, Val, Met, Phe, or Tyr.

<221> VARIANT
<222> (7)...(7)
<223> Arg can be Ser, Thr, Ala, or Cys.

<221> VARIANT
<222> (8)...(9)
<223> Xaa can be any amino acid.

<221> VARIANT
<222> (11)...(11)
<223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.

<221> VARIANT
<222> (12)...(12)
<223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.

<221> VARIANT
<222> (13)...(13)
<223> Leu can be Ile, Val, Met, Phe, Tyr, or Cys.

<400> 9
Leu Xaa His Xaa Asp Leu Arg Xaa Xaa Asn Leu Leu Leu
 1               5                  10
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<210> 10
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence for tyrosine kinase
      phosphorylation site (Prosite Accession No.
      PS00007)

<221> VARIANT
<222> 1
<223> Arg can be Lys.

<221> VARIANT
<222> 2
<223> Xaa can be any amino acid and can be two or three
      amino acids

<221> VARIANT
<222> 3
<223> Asp can be Glu.

<221> VARIANT
<222> 4
<223> Xaa can be any amino acid and can be two or three
      amino acids

<221> PHOSPHORYLATION
<222> 5

<400> 10
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 1               5
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